Title: US-10-787-267A-11

RESULT 11
AR204683
LOCUS AR204683 1503 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 6 from patent US 6368793.
ACCESSION AR204683
VERSION AR204683.1 GI:21502072
KEYWORDS .
SOURCE Unknown.
  ORGANISM Unknown.
  Unclassified.
REFERENCE 1 (bases 1 to 1503)
  AUTHORS Hoch,J. and Dartois,V.
  TITLE Metabolic selection methods
  JOURNAL Patent: US 6368793-A 6 09-APR-2002;
FEATURES Location/Qualifiers
  source 1. .1503
  /organism="unknown"
  /mol_type="unassigned DNA"
ORIGIN

  Query Match 2.3%; Score 34; DB 6; Length 1503;
  Best Local Similarity 100.0%; Pred. No. 6e-06;
  Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1467 ATGAGCAAGAAACAGGCCTTCTGGCTGGGTATTG 1500
  ||||||||||||||||||||||||||||||||||
Db 1 ATGAGCAAGAAACAGGCCTTCTGGCTGGGTATTG 34

Title: US-10-787-267A-11

RESULT 2
US-09-172-952-19
; Sequence 19, Application US/09172952
; Patent No. 6368793
; GENERAL INFORMATION:
; APPLICANT: Hoch, James
; APPLICANT: Dartois, Veronique
; TITLE OF INVENTION: METABOLIC SELECTION METHODS
; FILE REFERENCE: 234/191
; CURRENT APPLICATION NUMBER: US/09/172,952
; CURRENT FILING DATE: 1998-10-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 9334
; TYPE: DNA
; ORGANISM: yia
US-09-172-952-19

  Query Match 100.0%; Score 1500; DB 3; Length 9334;
  Best Local Similarity 100.0%; Pred. No. 0;
  Matches 1500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTAAAACAAGCACAATAATAATAATCACCTTCATCACCAGAATATTTTTAATATTACGAG 60
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Qy 61 ACTATAAAGATGAATATAACCTCTAACTCTACAACCAAAGATATACCGCGCCAGCGCTGG 120
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Qy 121 TTAAGAATCATTCCGCCTATACTGATCACTTGTATTATTTCTTATATGGACCGGGTCAAT 180
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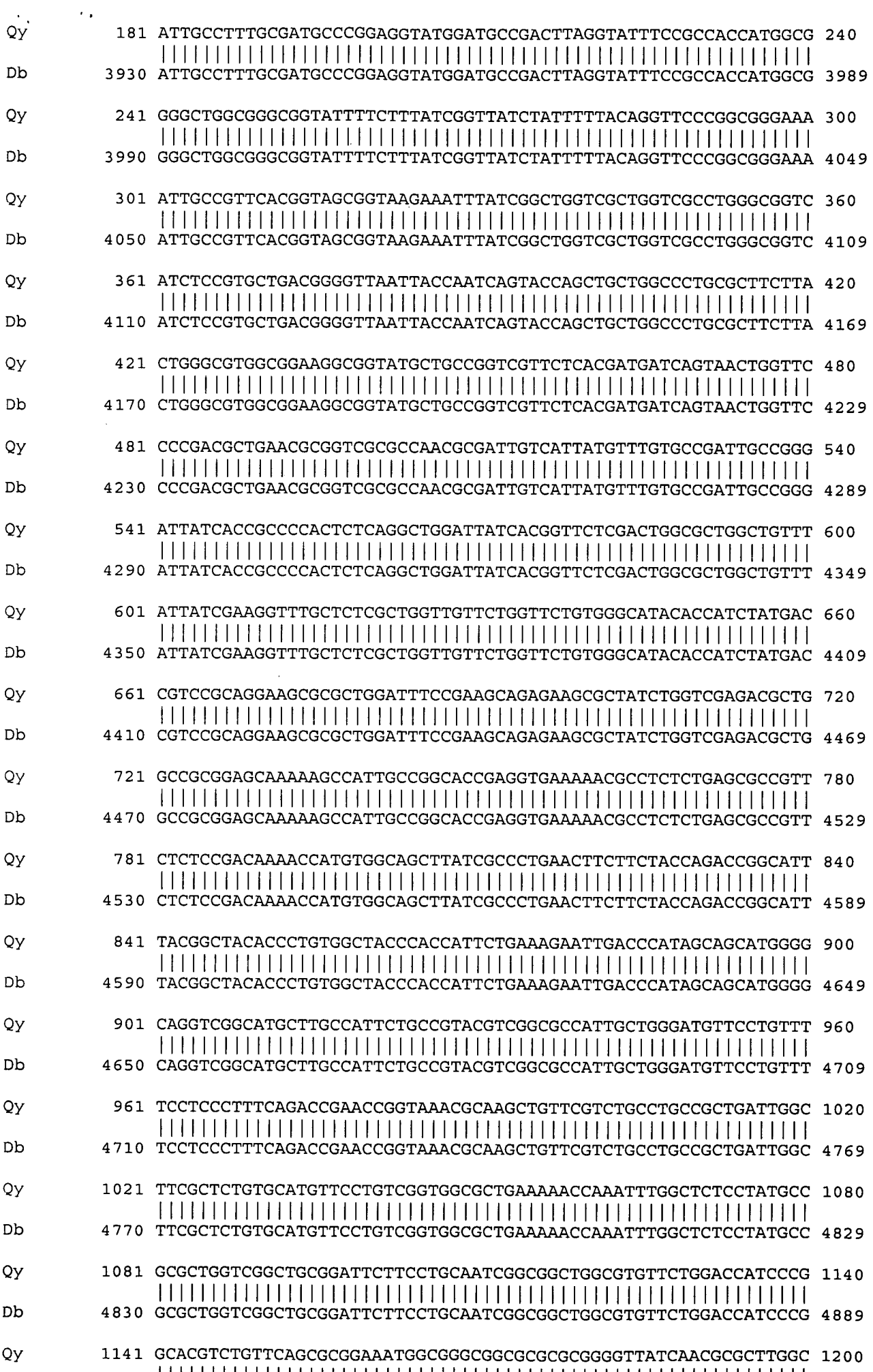
Qy 181 ATTGCCTTTGCGATGCCCGGAGGTATGGATGCCGACTTAGGTATTTCCGCCACCATGGCG 240
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Qy 241 GGGCTGGCGGGCGGTATTTTCTTTATCGGTTATCTATTTTTACAGGTTCCCGGCGGGAAA 300
Db 3990 GGGCTGGCGGGCGGTATTTTCTTTATCGGTTATCTATTTTTACAGGTTCCCGGCGGGAAA 4049
Qy 301 ATTGCCGTTCACGGTAGCGGTAAGAAATTTATCGGCTGGTCGCTGGTCGCCTGGGCGGTC 360
Db 4050 ATTGCCGTTCACGGTAGCGGTAAGAAATTTATCGGCTGGTCGCTGGTCGCCTGGGCGGTC 4109
Qy 361 ATCTCCGTGCTGACGGGGTTAATTACCAATCAGTACCAGCTGCTGGCCCTGCGCTTCTTA 420
Db 4110 ATCTCCGTGCTGACGGGGTTAATTACCAATCAGTACCAGCTGCTGGCCCTGCGCTTCTTA 4169
Qy 421 CTGGGCGTGGCGGAAGGCGGTATGCTGCCGGTCGTTCTCACGATGATCAGTAACTGGTTC 480
Db 4170 CTGGGCGTGGCGGAAGGCGGTATGCTGCCGGTCGTTCTCACGATGATCAGTAACTGGTTC 4229
Qy 481 CCCGACGCTGAACGCGGTCGCGCCAACGCGATTGTCATTATGTTTGTGCCGATTGCCGGG 540
Db 4230 CCCGACGCTGAACGCGGTCGCGCCAACGCGATTGTCATTATGTTTGTGCCGATTGCCGGG 4289
Qy 541 ATTATCACCGCCCCACTCTCAGGCTGGATTATCACGGTTCTCGACTGGCGCTGGCTGTTT 600
Db 4290 ATTATCACCGCCCCACTCTCAGGCTGGATTATCACGGTTCTCGACTGGCGCTGGCTGTTT 4349
Qy 601 ATTATCGAAGGTTTGCTCTCGCTGGTTGTTCTGGTTCTGTGGGCATACACCATCTATGAC 660
Db 4350 ATTATCGAAGGTTTGCTCTCGCTGGTTGTTCTGGTTCTGTGGGCATACACCATCTATGAC 4409
Qy 661 CGTCCGCAGGAAGCGCGCTGGATTTCCGAAGCAGAGAAGCGCTATCTGGTCGAGACGCTG 720
Db 4410 CGTCCGCAGGAAGCGCGCTGGATTTCCGAAGCAGAGAAGCGCTATCTGGTCGAGACGCTG 4469
Qy 721 GCCGCGGAGCAAAAAGCCATTGCCGGCACCGAGGTGAAAAACGCCTCTCTGAGCGCCGTT 780
Db 4470 GCCGCGGAGCAAAAAGCCATTGCCGGCACCGAGGTGAAAAACGCCTCTCTGAGCGCCGTT 4529
Qy 781 CTCTCCGACAAAACCATGTGGCAGCTTATCGCCCTGAACTTCTTCTACCAGACCGGCATT 840
Db 4530 CTCTCCGACAAAACCATGTGGCAGCTTATCGCCCTGAACTTCTTCTACCAGACCGGCATT 4589
Qy 841 TACGGCTACACCCTGTGGCTACCCACCATTCTGAAAGAATTGACCCATAGCAGCATGGGG 900
Db 4590 TACGGCTACACCCTGTGGCTACCCACCATTCTGAAAGAATTGACCCATAGCAGCATGGGG 4649
Qy 901 CAGGTCGGCATGCTTGCCATTCTGCCGTACGTCGGCGCCATTGCTGGGATGTTCCTGTTT 960
Db 4650 CAGGTCGGCATGCTTGCCATTCTGCCGTACGTCGGCGCCATTGCTGGGATGTTCCTGTTT 4709
Qy 961 TCCTCCCTTTCAGACCGAACCGGTAAACGCAAGCTGTTCGTCTGCCTGCCGCTGATTGGC 1020
Db 4710 TCCTCCCTTTCAGACCGAACCGGTAAACGCAAGCTGTTCGTCTGCCTGCCGCTGATTGGC 4769
Qy 1021 TTCGCTCTGTGCATGTTCCTGTCGGTGGCGCTGAAAAACCAAATTTGGCTCTCCTATGCC 1080
Db 4770 TTCGCTCTGTGCATGTTCCTGTCGGTGGCGCTGAAAAACCAAATTTGGCTCTCCTATGCC 4829
Qy 1081 GCGCTGGTCGGCTGCGGATTCTTCCTGCAATCGGCGGCTGGCGTGTTCTGGACCATCCCG 1140
Db 4830 GCGCTGGTCGGCTGCGGATTCTTCCTGCAATCGGCGGCTGGCGTGTTCTGGACCATCCCG 4889
Qy 1141 GCACGTCTGTTCAGCGCGGAAATGGCGGGCGGCGCGCGCGGGGTTATCAACGCGCTTGGC 1200

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Db      4890 GCACGTCTGTTCAGCGCGGAAATGGCGGGCGGCGCGCGCGGGGTTATCAACGCGCTTGGC 4949

Qy      1201 AACCTCGGCGGATTTTGTGGCCCTTATGCGGTCGGGGTGCTGATCACGTTGTACAGCAAA 1260
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Db      4950 AACCTCGGCGGATTTTGTGGCCCTTATGCGGTCGGGGTGCTGATCACGTTGTACAGCAAA 5009

Qy      1261 GACGCTGGCGTCTATTGCCTGGCGATCTCCCTGGCGCTGGCCGCGCTGATGGCGCTGCTG 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5010 GACGCTGGCGTCTATTGCCTGGCGATCTCCCTGGCGCTGGCCGCGCTGATGGCGCTGCTG 5069

Qy      1321 CTGCCGGCGAAATGCGATGCCGGTGCTGCGCCGGTAAAGACGATAAATCCACATAAACGC 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5070 CTGCCGGCGAAATGCGATGCCGGTGCTGCGCCGGTAAAGACGATAAATCCACATAAACGC 5129

Qy      1381 ACTGCGTAAACTCGAGCCCGGCGGCGCTGCGCCTGCCGGGCCTGCGAAATATGCCGGGTT 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5130 ACTGCGTAAACTCGAGCCCGGCGGCGCTGCGCCTGCCGGGCCTGCGAAATATGCCGGGTT 5189

Qy      1441 CACCCGGTAACAATGAGATGCGAAAGATGAGCAAGAAACAGGCCTTCTGGCTGGGTATTG 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5190 CACCCGGTAACAATGAGATGCGAAAGATGAGCAAGAAACAGGCCTTCTGGCTGGGTATTG 5249


Title:          US-10-787-267A-11

RESULT 3
US-09-172-952-5
; Sequence 5, Application US/09172952
; Patent No. 6368793
; GENERAL INFORMATION:
;  APPLICANT: Hoch, James
;  APPLICANT:  Dartois, Veronique
;  TITLE OF INVENTION: METABOLIC SELECTION METHODS
;  FILE REFERENCE: 234/191
;  CURRENT APPLICATION NUMBER: US/09/172,952
;  CURRENT FILING DATE:  1998-10-14
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
;   LENGTH: 1317
;   TYPE: DNA
;   ORGANISM: yia x2
US-09-172-952-5

  Query Match             87.8%;  Score 1317;  DB 3;  Length 1317;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1317;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         70 ATGAATATAACCTCTAACTCTACAACCAAAGATATACCGCGCCAGCGCTGGTTAAGAATC 129
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAATATAACCTCTAACTCTACAACCAAAGATATACCGCGCCAGCGCTGGTTAAGAATC 60

Qy        130 ATTCCGCCTATACTGATCACTTGTATTATTTCTTATATGGACCGGGTCAATATTGCCTTT 189
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATTCCGCCTATACTGATCACTTGTATTATTTCTTATATGGACCGGGTCAATATTGCCTTT 120

Qy        190 GCGATGCCCGGAGGTATGGATGCCGACTTAGGTATTTCCGCCACCATGGCGGGGCTGGCG 249
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCGATGCCCGGAGGTATGGATGCCGACTTAGGTATTTCCGCCACCATGGCGGGGCTGGCG 180

Qy        250 GGCGGTATTTTCTTTATCGGTTATCTATTTTTACAGGTTCCCGGCGGGAAAATTGCCGTT 309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGCGGTATTTTCTTTATCGGTTATCTATTTTTACAGGTTCCCGGCGGGAAAATTGCCGTT 240

Qy        310 CACGGTAGCGGTAAGAAATTTATCGGCTGGTCGCTGGTCGCCTGGGCGGTCATCTCCGTG 369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CACGGTAGCGGTAAGAAATTTATCGGCTGGTCGCTGGTCGCCTGGGCGGTCATCTCCGTG 300
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Qy        370 CTGACGGGGTTAATTACCAATCAGTACCAGCTGCTGGCCCTGCGCTTCTTACTGGGCGTG 429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTGACGGGGTTAATTACCAATCAGTACCAGCTGCTGGCCCTGCGCTTCTTACTGGGCGTG 360

Qy        430 GCGGAAGGCGGTATGCTGCCGGTCGTTCTCACGATGATCAGTAACTGGTTCCCCGACGCT 489
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCGGAAGGCGGTATGCTGCCGGTCGTTCTCACGATGATCAGTAACTGGTTCCCCGACGCT 420

Qy        490 GAACGCGGTCGCGCCAACGCGATTGTCATTATGTTTGTGCCGATTGCCGGGATTATCACC 549
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Db        421 GAACGCGGTCGCGCCAACGCGATTGTCATTATGTTTGTGCCGATTGCCGGGATTATCACC 480

Qy        550 GCCCCACTCTCAGGCTGGATTATCACGGTTCTCGACTGGCGCTGGCTGTTTATTATCGAA 609
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCCCACTCTCAGGCTGGATTATCACGGTTCTCGACTGGCGCTGGCTGTTTATTATCGAA 540

Qy        610 GGTTTGCTCTCGCTGGTTGTTCTGGTTCTGTGGGCATACACCATCTATGACCGTCCGCAG 669
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGTTTGCTCTCGCTGGTTGTTCTGGTTCTGTGGGCATACACCATCTATGACCGTCCGCAG 600

Qy        670 GAAGCGCGCTGGATTTCCGAAGCAGAGAAGCGCTATCTGGTCGAGACGCTGGCCGCGGAG 729
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GAAGCGCGCTGGATTTCCGAAGCAGAGAAGCGCTATCTGGTCGAGACGCTGGCCGCGGAG 660

Qy        730 CAAAAAGCCATTGCCGGCACCGAGGTGAAAAACGCCTCTCTGAGCGCCGTTCTCTCCGAC 789
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAAAAAGCCATTGCCGGCACCGAGGTGAAAAACGCCTCTCTGAGCGCCGTTCTCTCCGAC 720

Qy        790 AAAACCATGTGGCAGCTTATCGCCCTGAACTTCTTCTACCAGACCGGCATTTACGGCTAC 849
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Db        721 AAAACCATGTGGCAGCTTATCGCCCTGAACTTCTTCTACCAGACCGGCATTTACGGCTAC 780

Qy        850 ACCCTGTGGCTACCCACCATTCTGAAAGAATTGACCCATAGCAGCATGGGGCAGGTCGGC 909
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Qy        910 ATGCTTGCCATTCTGCCGTACGTCGGCGCCATTGCTGGGATGTTCCTGTTTTCCTCCCTT 969
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Qy        970 TCAGACCGAACCGGTAAACGCAAGCTGTTCGTCTGCCTGCCGCTGATTGGCTTCGCTCTG 1029
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Db        901 TCAGACCGAACCGGTAAACGCAAGCTGTTCGTCTGCCTGCCGCTGATTGGCTTCGCTCTG 960

Qy       1030 TGCATGTTCCTGTCGGTGGCGCTGAAAAACCAAATTTGGCTCTCCTATGCCGCGCTGGTC 1089
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGCATGTTCCTGTCGGTGGCGCTGAAAAACCAAATTTGGCTCTCCTATGCCGCGCTGGTC 1020

Qy       1090 GGCTGCGGATTCTTCCTGCAATCGGCGGCTGGCGTGTTCTGGACCATCCCGGCACGTCTG 1149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGCTGCGGATTCTTCCTGCAATCGGCGGCTGGCGTGTTCTGGACCATCCCGGCACGTCTG 1080

Qy       1150 TTCAGCGCGGAAATGGCGGGCGGCGCGCGCGGGGTTATCAACGCGCTTGGCAACCTCGGC 1209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TTCAGCGCGGAAATGGCGGGCGGCGCGCGCGGGGTTATCAACGCGCTTGGCAACCTCGGC 1140

Qy       1210 GGATTTTGTGGCCCTTATGCGGTCGGGGTGCTGATCACGTTGTACAGCAAAGACGCTGGC 1269
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Db       1141 GGATTTTGTGGCCCTTATGCGGTCGGGGTGCTGATCACGTTGTACAGCAAAGACGCTGGC 1200

Qy       1270 GTCTATTGCCTGGCGATCTCCCTGGCGCTGGCCGCGCTGATGGCGCTGCTGCTGCCGGCG 1329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GTCTATTGCCTGGCGATCTCCCTGGCGCTGGCCGCGCTGATGGCGCTGCTGCTGCCGGCG 1260

Qy       1330 AAATGCGATGCCGGTGCTGCGCCGGTAAAGACGATAAATCCACATAAACGCACTGCG 1386
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Db      1261 AAATGCGATGCCGGTGCTGCGCCGGTAAAGACGATAAATCCACATAAACGCACTGCG 1317


Title:          US-10-787-267A-11

RESULT 4
US-09-172-952-6
; Sequence 6, Application US/09172952
; Patent No. 6368793
; GENERAL INFORMATION:
;  APPLICANT: Hoch, James
;  APPLICANT:  Dartois, Veronique
;  TITLE OF INVENTION: METABOLIC SELECTION METHODS
;  FILE REFERENCE: 234/191
;  CURRENT APPLICATION NUMBER: US/09/172,952
;  CURRENT FILING DATE:  1998-10-14
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
;   LENGTH: 1503
;   TYPE: DNA
;   ORGANISM: lyxk
US-09-172-952-6

  Query Match             2.3%;  Score 34;  DB 3;  Length 1503;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-07;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db             1 ATGAGCAAGAAACAGGCCTTCTGGCTGGGTATTG 34


Title:          US-10-787-267A-11

RESULT 9
US-09-902-540-7050
; Sequence 7050, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 7050
;   LENGTH: 1095
;   TYPE: DNA
;   ORGANISM: Myxococcus xanthus
US-09-902-540-7050

  Query Match             1.4%;  Score 21;  DB 3;  Length 1095;
  Best Local Similarity   100.0%;  Pred. No. 3.2;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        233 CCATGGCGGGGCTGGCGGGCG 253
              |||||||||||||||||||||
Db        770 CCATGGCGGGGCTGGCGGGCG 790


Title:          US-10-787-267A-11
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RESULT 10
US-09-902-540-627
; Sequence 627, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 627
; LENGTH: 4835
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-627

Query Match 1.4%; Score 21; DB 3; Length 4835;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Title: US-10-787-267A-11

RESULT 10
AQ183262
LOCUS AQ183262 402 bp DNA linear GSS 01-NOV-1998
DEFINITION HS_3140_B2_G12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3140 Col=24 Row=N, genomic survey sequence.
ACCESSION AQ183262
VERSION AQ183262.1 GI:3580629
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 402)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
PUBMED 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3140 row: N column: 24
Class: BAC ends
High quality sequence stop: 402.

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FEATURES             Location/Qualifiers
     source          1. .402
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="Plate=3140 Col=24 Row=N"
                     /sex="male"
                     /clone_lib="CIT Approved Human Genomic Sperm Library D"
                     /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
                     E-Coli DH10B"
ORIGIN
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Query Match 1.4%; Score 21; DB 9; Length 402;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          74 ATATAACCTCTAACTCTACAA 94
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Db         104 ATATAACCTCTAACTCTACAA 124
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Title: US-10-787-267A-12

RESULT 1
US-09-172-952-14
; Sequence 14, Application US/09172952
; Patent No. 6368793
; GENERAL INFORMATION:
; APPLICANT: Hoch, James
; APPLICANT: Dartois, Veronique
; TITLE OF INVENTION: METABOLIC SELECTION METHODS
; FILE REFERENCE: 234/191
; CURRENT APPLICATION NUMBER: US/09/172,952
; CURRENT FILING DATE: 1998-10-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 439
; TYPE: PRT
; ORGANISM: YiaX2
US-09-172-952-14

Query Match 100.0%; Score 2254; DB 2; Length 439;
Best Local Similarity 100.0%; Pred. No. 2.3e-228;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MNITSNSTTKDIPRQRWLRIIPPILITCIISYMDRVNIAFAMPGGMDADLGISATMAGLA 60
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Db          1 MNITSNSTTKDIPRQRWLRIIPPILITCIISYMDRVNIAFAMPGGMDADLGISATMAGLA 60

Qy         61 GGIFFIGYLFLQVPGGKIAVHGSGKKFIGWSLVAWAVISVLTGLITNQYQLLALRFLLGV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGIFFIGYLFLQVPGGKIAVHGSGKKFIGWSLVAWAVISVLTGLITNQYQLLALRFLLGV 120

Qy        121 AEGGMLPVVLTMISNWFPDAERGRANAIVIMFVPIAGIITAPLSGWIITVLDWRWLFIIE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AEGGMLPVVLTMISNWFPDAERGRANAIVIMFVPIAGIITAPLSGWIITVLDWRWLFIIE 180

Qy        181 GLLSLVVLVLWAYTIYDRPQEARWISEAEKRYLVETLAAEQKAIAGTEVKNASLSAVLSD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GLLSLVVLVLWAYTIYDRPQEARWISEAEKRYLVETLAAEQKAIAGTEVKNASLSAVLSD 240

Qy        241 KTMWQLIALNFFYQTGIYGYTLWLPTILKELTHSSMGQVGMLAILPYVGAIAGMFLFSSL 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 KTMWQLIALNFFYQTGIYGYTLWLPTILKELTHSSMGQVGMLAILPYVGAIAGMFLFSSL 300

Qy        301 SDRTGKRKLFVCLPLIGFALCMFLSVALKNQIWLSYAALVGCGFFLQSAAGVFWTIPARL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 SDRTGKRKLFVCLPLIGFALCMFLSVALKNQIWLSYAALVGCGFFLQSAAGVFWTIPARL 360

Qy        361 FSAEMAGGARGVINALGNLGGFCGPYAVGVLITLYSKDAGVYCLAISLALAALMALLLPA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 FSAEMAGGARGVINALGNLGGFCGPYAVGVLITLYSKDAGVYCLAISLALAALMALLLPA 420

Qy        421 KCDAGAAPVKTINPHKRTA 439
              ||||||||||||||||||
Db        421 KCDAGAAPVKTINPHKRTA 439
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